

EXHIBIT A

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: PF0148_3CPA_SEQIDN01 289 aa
 Sequence 2: gi4583152 282 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 99
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score:3912
 Alignment Score 1827
 CLUSTAL-Alignment file created [baaTpaykK.aln]
 CLUSTAL W (1.7) multiple sequence alignment

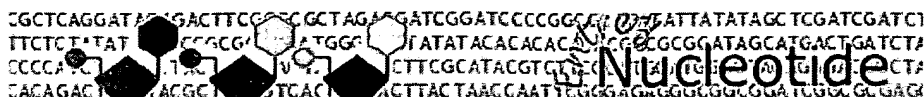
PF0148_3CPA_SEQIDN01	MSGFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYADKDV FHMVVEVPRWSNAKMEI
gi4583152	----STEERAAAFSLEYRVFLKNEKGQYISPFHDIPIYADKDV FHMVVEVPRWSNAKMEI

PF0148_3CPA_SEQIDN01	ATKDPLNPIKQDVKKGKRLRYVANLFPYKGYIWNYGAIPTWEDPGHNDKHTGCCGDNDPI
gi4583152	ATKDPLNPIKQDVKKGKRLRYVANLFPYKGYIWNYGAIPTWEDPGHNDKHTGCCGDNDPI

PF0148_3CPA_SEQIDN01	DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP
gi4583152	DVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKRLKP

PF0148_3CPA_SEQIDN01	GYLEATVDWFRRYKVPDGKPENEFNAEFKDKDFAIDI IKSTHDHWKALVTKKTNGKGI
gi4583152	GYLEATVDWFRRYKVPDGKPENEFNAEFKDKDFAIDI IKSTHDHWKALVTKKTNGKGI

PF0148_3CPA_SEQIDN01	SCMNTTLESSEPFKCDPDAARAIVDALPPPCESACTVPTDVKWFHHQKN
gi4583152	SCMNTTLESSEPFKCDPDAARAIVDALPPPCESACTVPTDVKWFHH---



1: AF108211. Homo sapiens cyto...[gi:4583152] [Links](#)

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1 agcaccgagg agcgcgcggc ggccttctcc ctggagtacc gagtcttctt caaaaatgag
61 aaaggacaat atatatctcc atttcatgat attccaattt atgcagataa ggatgtgttt
121 cacatggtag ttgaagtacc acgctggtct aatgcaaaaa tggagattgc tacaaaggac
181 cctttaaacc ctattaacaa agatgtgaaa aaaggaaaac ttgcctatgt tgcgaatttg

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241 ttcccgata aaggatat ctggaactat ggtgccatcc ctcagacttg ggaagaccca
301 gggcacaatg ataaacatac tggctgttgt ggtgacaatg acccaattga tgtgtgtgaa
361 attggaagca aggtatgtgc aagaggtgaa ataattggcg tgaaagttct aggcataattg
421 gctatgattg acgaagggga aaccgactgg aaagtcattg ccattaatgt ggatgaccc
481 gatgcagcca attataatga tatcaatgat gtcaaacggc tgaaacctgg ctacttagaa
541 gctactgtgg actggttttag aagggtataag gttcctgatg gaaaaccaga aaatgagttt
601 gcgtttaatg cagaatttaa agataaggac tttgccattg atattattaa aagcactcat
661 gaccattgga aagcattagt gactaagaaa acgaatggaa aaggaatcag ttgcatgaat
721 acaactttgt ctgagagccc cttcaagtgt gatcctgatg ctgccagagc cattgtggat
781 gctttaccac caccctgtga atctgcgtgc acagtaccaa cagacgtgga taagtggttc
841 catcac

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